

Ala Ala Tyr Glu Asp Gly Trp Tyr Ala Leu Lys Trp Val Thr Ser His
130 135 140

Ser Thr Asn Asn Asn Lys Pro Thr Asn Ala Asp Pro Trp Leu Ile Lys
145 150 155 160

His Gly Asp Phe Asn Arg Phe Tyr Ile Gly Gly Asp Thr Ser Gly Ala
165 170 175

Asn Ile Ala His Asn Ala Ala Leu Arg Val Gly Ala Glu Ala Leu Pro
180 185 190

Gly Gly Leu Arg Ile Ala Gly Val Leu Ser Ala Phe Pro Leu Phe Trp
195 200 205

Gly Ser Lys Pro Val Leu Ser Glu Pro Val Glu Gly His Glu Lys Ser
210 215 220

Ser Pro Met Gln Val Trp Asn Phe Val Tyr Pro Asp Ala Pro Gly Gly
225 230 235 240

Ile Asp Asn Pro Leu Ile Asn Pro Leu Ala Pro Gly Ala Pro Asn Leu
245 250 255

Ala Thr Leu Gly Cys Pro Lys Met Leu Val Phe Val Ala Gly Lys Asp
260 265 270

Asp Leu Arg Asp Arg Gly Ile Trp Tyr Tyr Glu Ala Val Lys Glu Ser
275 280 285

Gly Trp Lys Gly Asp Val Glu Leu Ala Gln Tyr Glu Gly Glu Glu His
290 295 300

Cys Phe Gln Ile Tyr His Pro Glu Thr Glu Asn Ser Lys Asp Leu Ile
305 310 315 320

Gly Arg Ile Ala Ser Phe Leu Val
325

<210> 2

<211> 1178

<212> DNA

<213> Glycyrrhiza echinata

<220>

<221> CDS

<222> (23)..(1006)

<400> 2

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aaa gag ata gac agg gag ctt cct cct ctt ctc cgg gtc tac aaa gat 100
Lys Glu Ile Asp Arg Glu Leu Pro Pro Leu Leu Arg Val Tyr Lys Asp
15 20 25

gga acc gtg gag cga ttc cta ggc tca tcg ttt gta cca cct tcc cct 148
Gly Thr Val Glu Arg Phe Leu Gly Ser Ser Phe Val Pro Pro Ser Pro
30 35 40

gaa gac ccc gaa aca ggg gtt tcc acg aaa gac ata gta atc tca gaa	196
Glu Asp Pro Glu Thr Gly Val Ser Thr Lys Asp Ile Val Ile Ser Glu	
45 50 55	
aac ccc acc atc tct gct cgc gtt tac ctt cca aaa ctg aac aac acc	244
Asn Pro Thr Ile Ser Ala Arg Val Tyr Leu Pro Lys Leu Asn Asn Thr	
60 65 70	
acc gag aag ctc cca atc ttg gtc tac tac cac ggc ggc gcg ttc tgc	292
Thr Glu Lys Leu Pro Ile Leu Val Tyr Tyr His Gly Gly Ala Phe Cys	
75 80 85 90	
ctc gaa tct gct ttc tcc ttc ctc cac caa cgc tac ctc aac atc gtt	340
Leu Glu Ser Ala Phe Ser Phe Leu His Gln Arg Tyr Leu Asn Ile Val	
95 100 105	
gct tcc aag gca aat gtt cta gta gtt tcc atc gag tac agg ctc gcc	388
Ala Ser Lys Ala Asn Val Leu Val Val Ser Ile Glu Tyr Arg Leu Ala	
110 115 120	
cca gaa cac cct ctt ccg gct gca tat gaa gat ggt tgg tat gct ctc	436
Pro Glu His Pro Leu Pro Ala Ala Tyr Glu Asp Gly Trp Tyr Ala Leu	
125 130 135	
aaa tgg gtc act tct cat tcc aca aac aac aac aaa ccc acc aac gct	484
Lys Trp Val Thr Ser His Ser Thr Asn Asn Asn Lys Pro Thr Asn Ala	
140 145 150	
gac cca tgg ttg atc aaa cac ggt gat ttc aac agg ttc tac atc ggg	532
Asp Pro Trp Leu Ile Lys His Gly Asp Phe Asn Arg Phe Tyr Ile Gly	
155 160 165 170	
ggg gac act tct ggt gca aac att gca cac aat gcg gct ctt cgt gtt	580
Gly Asp Thr Ser Gly Ala Asn Ile Ala His Asn Ala Ala Leu Arg Val	
175 180 185	
ggg gct gag gcc tta cct ggg ggg ctg aga ata gca ggg gta ctc tct	628
Gly Ala Glu Ala Leu Pro Gly Gly Leu Arg Ile Ala Gly Val Leu Ser	
190 195 200	
gct ttt cct ctg ttt tgg ggt tct aag cct gtt ttg tca gaa cct gtc	676
Ala Phe Pro Leu Phe Trp Gly Ser Lys Pro Val Leu Ser Glu Pro Val	
205 210 215	
gag ggg cat gag aag agc tca ccc atg caa gtt tgg aac ttt gtg tac	724
Glu Gly His Glu Lys Ser Ser Pro Met Gln Val Trp Asn Phe Val Tyr	
220 225 230	
cca gat gca cca ggt ggc ata gat aac cca cta atc aac cct ttg gca	772
Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Leu Ile Asn Pro Leu Ala	
235 240 245 250	
cct ggg gct cct aac ttg gcc aca ctt ggg tgt cca aag atg ttg gtc	820
Pro Gly Ala Pro Asn Leu Ala Thr Leu Gly Cys Pro Lys Met Leu Val	
255 260 265	

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ttt gtt gcg ggg aag gat gat ctt aga gac aga ggg att tgg tac tat      868
Phe Val Ala Gly Lys Asp Asp Leu Arg Asp Arg Gly Ile Trp Tyr Tyr
      270                      275                      280

gag gct gtg aag gaa agt ggg tgg aaa ggg gat gtg gaa ctt gct cag      916
Glu Ala Val Lys Glu Ser Gly Trp Lys Gly Asp Val Glu Leu Ala Gln
      285                      290                      295

tat gaa ggg gag gaa cat tgc ttc cag atc tac cat cct gaa act gag      964
Tyr Glu Gly Glu Glu His Cys Phe Gln Ile Tyr His Pro Glu Thr Glu
      300                      305                      310

aat tct aaa gat ctc atc ggt cgc atc gct tcc ttc ctt gtt      1006
Asn Ser Lys Asp Leu Ile Gly Arg Ile Ala Ser Phe Leu Val
      315                      320                      325

tgaacacaca gctagacttc gggttcatta ttactagtat gtgattttgt ttgattaatg 1066

ttttgtcatc aattgatggg taataaattg gattagggta ctagggttcc tgaatcatgc 1126

tcaattttac ttttctgta ctattacttg tttatgaaag aattaatggc at      1178

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<212> PRT
<213> Glycine max

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Ser Pro Glu Asp Pro Gln Thr Gly Val Ser Ser Lys Asp Ile Val Ile
      35              40              45

Ala Asp Asn Pro Tyr Val Ser Ala Arg Ile Phe Leu Pro Lys Ser His
      50              55              60

His Thr Asn Asn Lys Leu Pro Ile Phe Leu Tyr Phe His Gly Gly Ala
      65              70              75              80

Phe Cys Val Glu Ser Ala Phe Ser Phe Phe Val His Arg Tyr Leu Asn
      85              90              95

Ile Leu Ala Ser Glu Ala Asn Ile Ile Ala Ile Ser Val Asp Phe Arg
      100             105             110

Leu Leu Pro His His Pro Ile Pro Ala Ala Tyr Glu Asp Gly Trp Thr
      115             120             125

Thr Leu Lys Trp Ile Ala Ser His Ala Asn Asn Thr Asn Thr Thr Asn
      130             135             140

Pro Glu Pro Trp Leu Leu Asn His Ala Asp Phe Thr Lys Val Tyr Val
      145             150             155             160

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Gly Gly Glu Thr Ser Gly Ala Asn Ile Ala His Asn Leu Leu Leu Arg
 165 170 175
 Ala Gly Asn Glu Ser Leu Pro Gly Asp Leu Lys Ile Leu Gly Gly Leu
 180 185 190
 Leu Cys Cys Pro Phe Phe Trp Gly Ser Lys Pro Ile Gly Ser Glu Ala
 195 200 205
 Val Glu Gly His Glu Gln Ser Leu Ala Met Lys Val Trp Asn Phe Ala
 210 215 220
 Cys Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Trp Ile Asn Pro Cys
 225 230 235 240
 Val Pro Gly Ala Pro Ser Leu Ala Thr Leu Ala Cys Ser Lys Leu Leu
 245 250 255
 Val Thr Ile Thr Gly Lys Asp Glu Phe Arg Asp Arg Asp Ile Leu Tyr
 260 265 270
 His His Thr Val Glu Gln Ser Gly Trp Gln Gly Glu Leu Gln Leu Phe
 275 280 285
 Asp Ala Gly Asp Glu Glu His Ala Phe Gln Leu Phe Lys Pro Glu Thr
 290 295 300
 His Leu Ala Lys Ala Met Ile Lys Arg Leu Ala Ser Phe Leu Val
 305 310 315

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 <211> 960
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(957)

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 aag gat ggc agc gtg gag cgt ctt cta agc tct gaa aac gtg gca gcc 96
 Lys Asp Gly Ser Val Glu Arg Leu Leu Ser Ser Glu Asn Val Ala Ala
 20 25 30
 tcc cct gaa gat ccc caa act gga gtc tca tcc aaa gac ata gtc atc 144
 Ser Pro Glu Asp Pro Gln Thr Gly Val Ser Ser Lys Asp Ile Val Ile
 35 40 45
 gca gac aac ccc tac gtc tcc gct cgc att ttc ctt ccc aaa tcc cac 192
 Ala Asp Asn Pro Tyr Val Ser Ala Arg Ile Phe Leu Pro Lys Ser His
 50 55 60

cac act aac aac aaa ctc ccc atc ttc ctc tac ttc cac ggt ggc gcc	240
His Thr Asn Asn Lys Leu Pro Ile Phe Leu Tyr Phe His Gly Gly Ala	
65 70 75 80	
ttt tgc gtc gaa tcc gcc ttc tcc ttt ttc gtc cac cgc tat ctc aac	288
Phe Cys Val Glu Ser Ala Phe Ser Phe Phe Val His Arg Tyr Leu Asn	
85 90 95	
atc ttg gcc tca gaa gcc aac ata ata gcc atc tcc gtc gac ttc aga	336
Ile Leu Ala Ser Glu Ala Asn Ile Ile Ala Ile Ser Val Asp Phe Arg	
100 105 110	
ctc ctc cca cac cac cct atc cct gct gcc tac gaa gac ggt tgg acc	384
Leu Leu Pro His His Pro Ile Pro Ala Ala Tyr Glu Asp Gly Trp Thr	
115 120 125	
acc ctc aaa tgg att gct tcc cac gcc aac aac acc aac acc aac aac	432
Thr Leu Lys Trp Ile Ala Ser His Ala Asn Asn Thr Asn Thr Thr Asn	
130 135 140	
ccg gag cca tgg cta ctc aac cac gcc gac ttc acc aaa gtc tac gta	480
Pro Glu Pro Trp Leu Leu Asn His Ala Asp Phe Thr Lys Val Tyr Val	
145 150 155 160	
gga ggt gaa acc agc ggt gct aac atc gca cac aac ctg ctt ttg cgt	528
Gly Gly Glu Thr Ser Gly Ala Asn Ile Ala His Asn Leu Leu Leu Arg	
165 170 175	
gca ggt aac gaa tcc ctc ccc ggg gat ctg aaa ata ttg ggt gga tta	576
Ala Gly Asn Glu Ser Leu Pro Gly Asp Leu Lys Ile Leu Gly Gly Leu	
180 185 190	
cta tgc tgc ccc ttc ttc tgg ggc tcg aag cca att ggg tcg gag gct	624
Leu Cys Cys Pro Phe Phe Trp Gly Ser Lys Pro Ile Gly Ser Glu Ala	
195 200 205	
gtt gag ggg cac gag cag agt ttg gcc atg aag gtc tgg aac ttt gcc	672
Val Glu Gly His Glu Gln Ser Leu Ala Met Lys Val Trp Asn Phe Ala	
210 215 220	
tgc cct gat gcc ccc ggt gga atc gat aac ccc tgg atc aac ccc tgt	720
Cys Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Trp Ile Asn Pro Cys	
225 230 235 240	
gtt cct ggg gca ccc tct ttg gcc act ctt gcc tgc tct aag ttg ctc	768
Val Pro Gly Ala Pro Ser Leu Ala Thr Leu Ala Cys Ser Lys Leu Leu	
245 250 255	
gtt act atc act ggc aaa gac gag ttc aga gac aga gat att ctc tac	816
Val Thr Ile Thr Gly Lys Asp Glu Phe Arg Asp Arg Asp Ile Leu Tyr	
260 265 270	
cac cac acc gtt gag caa agt ggc tgg caa ggt gaa ctt caa ctc ttt	864
His His Thr Val Glu Gln Ser Gly Trp Gln Gly Glu Leu Gln Leu Phe	
275 280 285	

gat gct ggc gat gag gag cat gct ttc cag ctc ttc aag cct gag act 912
 Asp Ala Gly Asp Glu Glu His Ala Phe Gln Leu Phe Lys Pro Glu Thr
 290 295 300

cat ctt gct aaa gcc atg atc aaa cgc ttg gct tct ttt ctg gtt tga 960
 His Leu Ala Lys Ala Met Ile Lys Arg Leu Ala Ser Phe Leu Val
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<210> 5
 <211> 25
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 5
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<210> 6
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 6
 agggatccat caaaccagaa aaga 24

<210> 7
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 7
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<210> 8
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 8
ctggatcctc aaacaaggaa ggaag

25

<210> 9
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 9
ggggcccga tccacggcga aggagatagt gaaag

35

<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 10
gggagctcga gtcaaaccag aaaagaagcc

30